



STIC Search Report

Biotech-Chem Library

STIC Database Tracking Number: 152115

TO: Nita M Minnifield
Location: REM-3C01&3C18
Art Unit: 1645

May 3, 2005

Case Serial Number: 09/642744

From: P. Sheppard
Location: Remsen Building
Phone: (571) 272-2529

sheppard@uspto.gov

Search Notes

*Reviewed
6-5-05*

152115

From: Chan, Christina
Sent: Friday, April 29, 2005 3:42 PM
To: Pak, Michael; STIC-Biotech/ChemLib
Cc: Minnifield, Nita
Subject: RE: approval for additional sequences to be searched

Importance: High

Please rush. Thanks Chris

Chris Chan

TC 1600 New Hire Training Coordinator and SPE 1644
(571)-272-0841
Remsen, 3E89

CRFE

-----Original Message-----

From: Pak, Michael
Sent: Friday, April 29, 2005 1:37 PM
To: Chan, Christina
Cc: Minnifield, Nita
Subject: RE: approval for additional sequences to be searched

Dear STIC,

Please search the multiple sequence search request set forth below.

Thanks,

Mike Pak

-----Original Message-----

From: Minnifield, Nita
Sent: Thursday, April 28, 2005 10:09 PM
To: Pak, Michael
Subject: approval for additional sequences to be searched

Michael,
09/642744

I have been asked to work on this application (originally not my case) since it is an AF that is overdue and Atty. is calling regarding response to the AF and his time is running out. All of the sequences were searched previously, but they need to be searched again because Applicant corrected some error that was in the RSL.

SEQ ID NO: 1, 6-17, 19-26 and 28. They are all peptides. I need a commercial and interference search done.

Your approval is greatly appreciated.

Please forward to Christina for RUSH approval.

STIC

STAFF USE ONLY

Searcher: _____
Searcher Phone: 2-_____
Date Searcher Picked up: _____
Date Completed: _____
Searcher Prep/Rev. Time: _____
Online Time: _____

Type of Search

NA#: _____ AA#: _____
Interference: _____ SPDI: _____
S/L: _____ Oligomer: _____
Encode/Transl: _____
Structure#: _____ Text: _____
Inventor: _____ Litigation: _____

Vendors and cost where applicable

STN: _____
DIALOG: _____
QUESTEL/ORBIT: _____
LEXIS/NEXIS: _____
SEQUENCE SYSTEM: _____
WWW/Internet: _____
Other(Specify): _____

09/642744

Please do a commercial and interference search on SEQ ID NO: 1, 6-17, 19-26 and 28. They are all peptides.

Please provide a paper copy of results.

Thanks,
Minnifield
71976
Art Unit 1645
Office REM-3C01
Mailbox REM-3C18
571-272-0860

STAFF USE ONLY

Searcher: _____
Searcher Phone: 2- _____
Date Searcher Picked up: _____
Date Completed: _____
Searcher Prep/Rev. Time: _____
Online Time: _____

Type of Search

NA#: _____ AA#: _____
Interference: _____ SPDI: _____
S/L: _____ Oligomer: _____
Encode/Transl: _____
Structure#: _____ Text: _____
Inventor: _____ Litigation: _____

Vendors and cost where applicable

STN: _____
DIALOG: _____
QUESTEL/ORBIT: _____
LEXIS/NEXIS: _____
SEQUENCE SYSTEM: _____
WWW/Internet: _____
Other(Specify): _____

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OM protein - protein search, using sw model

Run on: May 4, 2005, 13:00:51 ; Search time 93.3333 Seconds

(without alignments)
98.758 Million cell updates/sec

Title: US-09-642-744d-7

Sequence: 1 KNIRRIKRIHKKYG 18

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : 1: uniprot_sprot;*
2: uniprot_trembl;*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	55	61.1	160	1	SCS1_SHEEP
2	55	61.1	160	1	SCS2_SHEEP
3	52	57.8	146	2	09A1H3
4	49	54.4	2017	2	0675T1
5	48.5	53.9	314	2	065L76
6	48.5	53.9	324	2	062X75
7	48	53.3	255	2	09LJW2
8	48	53.3	500	1	TF3B_SCHPO
9	47	52.2	232	2	07MTQ1
10	47	52.2	581	2	06EBB6
11	47	52.2	3267	2	081B20
12	46	51.1	93	2	064D16
13	46	51.1	113	2	0703Z0
14	46	51.1	250	2	06L7F9
15	46	51.1	282	2	08DVR3
16	46	51.1	282	2	08B4C0
17	46	51.1	319	2	005804
18	46	51.1	343	2	076C22
19	46	51.1	807	1	HIS8_PHOHL
20	46	51.1	1774	2	0754J8
21	46	51.1	2084	2	081LJ6
22	45.5	50.6	208	1	TRP_NEMMA
23	45.5	50.6	208	1	TRP_NEMMA
24	45	50.0	182	2	0896E1
25	45	50.0	234	2	059264
26	45	50.0	308	2	08R2C7
27	45	50.0	420	1	PR11_HUMAN
28	45	50.0	609	2	072K21
29	45	50.0	609	2	08F908
30	45	50.0	647	2	062647
31	45	50.0	834	2	07RR10

ALIGNMENTS

RESULT 1	ID	SCS1_SHEEP	STANDARD	PRT	160 AA.	08iml2 plasmodium
AC	P49928	01-OCT-1996 (Rel. 34, Created)				08iml2 plasmodium
DT	01-OCT-1996 (Rel. 34, Last sequence update)					08iml2 plasmodium
DT	25-OCT-2004 (Rel. 45, Last annotation update)					08iml2 plasmodium
DE	Cathelin-related peptide SCS precursor 1 (Antibacterial peptide SMAP-29)					08iml2 plasmodium
DE	Ovis aries (sheep)					08iml2 plasmodium
OC	Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;					08iml2 plasmodium
OC	Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;					08iml2 plasmodium
OX	Caprinae; Ovis					08iml2 plasmodium
OX	NCBI_TaxID=9940;					08iml2 plasmodium
RP	SEQUENCE FROM N.A.					08iml2 plasmodium
RC	TISSUE=Bone marrow;					08iml2 plasmodium
RC	Medline=96140581; PubMed=8549789; DOI=10.1016/0014-5793(95)01390-3;					08iml2 plasmodium
RA	Maehoney M.M., Lee A.Y., Brezinski-Caliquiri D.J., Hutterer K.M.;					08iml2 plasmodium
RT	"Molecular analysis of the sheep cathelin family reveals a novel					08iml2 plasmodium
RT	antimicrobial peptide."					08iml2 plasmodium
RL	FEBS Lett. 377:519-522(1995).					08iml2 plasmodium
RN	[2]					08iml2 plasmodium
RP	SEQUENCE FROM N.A.					08iml2 plasmodium
RP	TISSUE=Liver;					08iml2 plasmodium
RA	Hutterer K.M., Maehoney M.M.;					08iml2 plasmodium
RL	Submitted (JUN-1996) to the EMBL/GenBank/DBJ databases.					08iml2 plasmodium
CC	- FUNCTION: Thermostable, broad spectrum, bactericidal agent.					08iml2 plasmodium
CC	- SUBCELLULAR LOCATION: Secreted.					08iml2 plasmodium
CC	- SIMILARITY: Belongs to the cathelicidin family.					08iml2 plasmodium
CC	-----					08iml2 plasmodium
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration					08iml2 plasmodium
CC	between the Swiss Institute of Bioinformatics and the EMBL outstation-					08iml2 plasmodium
CC	the European Bioinformatics Institute. There are no restrictions on its					08iml2 plasmodium
CC	use by non-profit institutions as long as its content is in no way					08iml2 plasmodium
CC	modified and this statement is not removed. Usage by and for commercial					08iml2 plasmodium
CC	entities requires a license agreement (See http://www.isb-sib.ch/announce/					08iml2 plasmodium
CC	or send an email to license@sib-sib.ch).					08iml2 plasmodium
CC	-----					08iml2 plasmodium
DR	EMBL; X92757; CAAG3412.1; -					08iml2 plasmodium
DR	EMBL; U06000; AAB89715.1; -					08iml2 plasmodium
DR	PDB; 1FRY; NMR; A-132-160.					08iml2 plasmodium
DR	InterPro; IPR001894; Cathelicidin.					08iml2 plasmodium
DR	Pfam; PF00666; Cathelicidin; 1.					08iml2 plasmodium
DR	ProDom; PD001838; Cathelicidin; 1.					08iml2 plasmodium
DR	PROSITE; PS00946; CATHELICIDINS_1; 1.					08iml2 plasmodium
DR	PROSITE; PS00947; CATHELICIDINS_2; 1.					08iml2 plasmodium
KW	3D structure; Antibiotic; Pyrolytic; Pyrolytic carboxylic acid; Signal.					08iml2 plasmodium
FT	SIGNAL	1	29			08iml2 plasmodium
FT	PROPEP	30	131			08iml2 plasmodium
FT	PEPTIDE	132	160			08iml2 plasmodium
FT	MOD_RES	30	30			08iml2 plasmodium
FT	DISULFID	86	97			08iml2 plasmodium

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OM protein - protein search, using sw model

Run on: May 4, 2005, 13:14:52 ; Search time 75 Seconds
(without alignments)
79.945 Million cell updates/sec

Title: US-09-642-744D-7

Perfect score: 90

Sequence: 1 KNIRRIIRKIHIKKYK 18

Scoring table: BLOSUM62

Gapop 10.0, Gapext 0.5

Searched: 1426032 seqs, 33106140 residues

Total number of hits satisfying chosen parameters: 1426032

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

Published Applications AA:
1: /cgn2_6/ptodata/1/pubppa/US07_PUBCOMB.pep.*
2: /cgn2_6/ptodata/1/pubppa/PTCT_NEW_PUB.pep.*
3: /cgn2_6/ptodata/1/pubppa/US06_NEW_PUB.pep.*
4: /cgn2_6/ptodata/1/pubppa/US06_PUBCOMB.pep.*
5: /cgn2_6/ptodata/1/pubppa/US07_PUBCOMB.pep.*
6: /cgn2_6/ptodata/1/pubppa/US07_NEW_PUB.pep.*
7: /cgn2_6/ptodata/1/pubppa/US08_PUBCOMB.pep.*
8: /cgn2_6/ptodata/1/pubppa/US08_NEW_PUB.pep.*
9: /cgn2_6/ptodata/1/pubppa/US09_PUBCOMB.pep.*
10: /cgn2_6/ptodata/1/pubppa/US09_NEW_PUB.pep.*
11: /cgn2_6/ptodata/1/pubppa/US09_PUBCOMB.pep.*
12: /cgn2_6/ptodata/1/pubppa/US09_NEW_PUB.pep.*
13: /cgn2_6/ptodata/1/pubppa/US10_PUBCOMB.pep.*
14: /cgn2_6/ptodata/1/pubppa/US10_NEW_PUB.pep.*
15: /cgn2_6/ptodata/1/pubppa/US10_PUBCOMB.pep.*
16: /cgn2_6/ptodata/1/pubppa/US10_NEW_PUB.pep.*
17: /cgn2_6/ptodata/1/pubppa/US10_PUBCOMB.pep.*
18: /cgn2_6/ptodata/1/pubppa/US11_NEW_PUB.pep.*
19: /cgn2_6/ptodata/1/pubppa/US60_NEW_PUB.pep.*
20: /cgn2_6/ptodata/1/pubppa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	90	100.0	18	14	US-10-060-102-10
2	90	100.0	18	14	US-10-060-102-11
3	90	100.0	18	15	US-10-721-839-10
4	90	100.0	18	15	US-10-721-839-11
5	88	97.8	18	9	US-09-840-009-2
6	88	97.8	18	9	US-09-840-009-9
7	88	97.8	18	9	US-09-840-009-16
8	88	97.8	18	9	US-09-840-009-23
9	88	97.8	18	9	US-09-840-009-30
10	88	97.8	18	14	US-10-060-102-9
11	88	97.8	18	14	US-10-060-102-12
12	88	97.8	18	15	US-10-721-839-9
13	88	97.8	18	15	US-10-721-839-12

14	88	97.8	29	14	US-10-060-102-8	Sequence 8, Appli
15	88	97.8	29	15	US-10-721-839-8	Sequence 8, Appli
16	83	92.2	18	9	US-09-840-009-4	Sequence 4, Appli
17	83	92.2	18	9	US-09-840-009-8	Sequence 8, Appli
18	83	92.2	18	9	US-09-840-009-11	Sequence 11, Appli
19	83	92.2	18	9	US-09-840-009-15	Sequence 15, Appli
20	83	92.2	18	9	US-09-840-009-18	Sequence 18, Appli
21	83	92.2	18	9	US-09-840-009-22	Sequence 22, Appli
22	83	92.2	18	9	US-09-840-009-25	Sequence 25, Appli
23	83	92.2	18	9	US-09-840-009-29	Sequence 29, Appli
24	83	92.2	18	14	US-10-060-102-25	Sequence 25, Appli
25	83	92.2	18	15	US-10-721-839-25	Sequence 25, Appli
26	82	91.1	18	9	US-09-840-009-5	Sequence 5, Appli
27	82	91.1	18	9	US-09-840-009-12	Sequence 12, Appli
28	82	91.1	18	9	US-09-840-009-19	Sequence 19, Appli
29	82	91.1	18	9	US-09-840-009-26	Sequence 26, Appli
30	81	90.0	18	9	US-09-840-009-6	Sequence 6, Appli
31	81	90.0	18	9	US-09-840-009-7	Sequence 7, Appli
32	81	90.0	18	9	US-09-840-009-13	Sequence 13, Appli
33	81	90.0	18	9	US-09-840-009-14	Sequence 14, Appli
34	81	90.0	18	9	US-09-840-009-20	Sequence 20, Appli
35	81	90.0	18	9	US-09-840-009-21	Sequence 21, Appli
36	81	90.0	18	9	US-09-840-009-27	Sequence 27, Appli
37	81	90.0	18	9	US-09-840-009-28	Sequence 28, Appli
38	80	88.9	18	9	US-09-840-009-3	Sequence 3, Appli
39	80	88.9	18	9	US-09-840-009-10	Sequence 10, Appli
40	80	88.9	18	9	US-09-840-009-17	Sequence 17, Appli
41	80	88.9	18	9	US-09-840-009-24	Sequence 24, Appli
42	80	88.9	18	9	US-09-840-009-31	Sequence 31, Appli
43	80	88.9	18	14	US-10-060-102-26	Sequence 26, Appli
44	80	88.9	18	14	US-10-077-624-17	Sequence 17, Appli
45	80	88.9	18	15	US-10-721-839-26	Sequence 26, Appli

ALIGNMENTS

RESULT 1
US-10-060-102-10
Sequence 10, Application US/10060102
Publication No. US20030022829A1
GENERAL INFORMATION:
APPLICANT: MAURY, WENDY
APPLICANT: STAPLETON, JACK
APPLICANT: ROLLER, RICHARD
APPLICANT: STINSKI, MARK
APPLICANT: MCCRAY, PAUL B.
TITLE OF INVENTION: NOVEL ANTIVIRAL ACTIVITIES OF PRIMATE THETA DEFENSINS AND MAMMALI
FILE REFERENCE: IOWA:035US
CURRENT APPLICATION NUMBER: US/10/060,102
CURRENT FILING DATE: 2002-02-22
PRIOR APPLICATION NUMBER: 60/309,368
PRIOR FILING DATE: 2001-08-01
PRIOR APPLICATION NUMBER: 60/265,270
PRIOR FILING DATE: 2001-01-30
NUMBER OF SEQ ID NOS: 32
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO: 10
LENGTH: 18
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-10-060-102-10

Query Match 100.0%; Score 90; DB 14; Length 18;
Best Local Similarity 100.0%; Pred. NO. 4.3e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 KNIRRIIRKIHIKKYK 18

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OM protein - protein search, using sw model

Run on: May 4, 2005, 13:02:32 ; Search time 25.6667 Seconds

(without alignments)
52.351 Million cell updates/sec

Title: US-09-642-744D-7

Sequence: 1 KNIRRIIRKIHIIKKYG 18

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA: *
1: /cgn2_6/ptodata/1/1aa/5A.COMB.pep: *
2: /cgn2_6/ptodata/1/1aa/5B.COMB.pep: *
3: /cgn2_6/ptodata/1/1aa/6A.COMB.pep: *
4: /cgn2_6/ptodata/1/1aa/6B.COMB.pep: *
5: /cgn2_6/ptodata/1/1aa/6C.COMB.pep: *
6: /cgn2_6/ptodata/1/1aa/6D.COMB.pep: *

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	88	97.8	18	US-09-840-009-2	Sequence 2, Appl
2	88	97.8	18	US-09-840-009-9	Sequence 9, Appl
3	88	97.8	18	US-09-840-009-16	Sequence 16, Appl
4	88	97.8	18	US-09-840-009-23	Sequence 23, Appl
5	88	97.8	18	US-09-840-009-30	Sequence 30, Appl
6	83	92.2	18	US-09-840-009-4	Sequence 4, Appl
7	83	92.2	18	US-09-840-009-8	Sequence 8, Appl
8	83	92.2	18	US-09-840-009-11	Sequence 11, Appl
9	83	92.2	18	US-09-840-009-15	Sequence 15, Appl
10	83	92.2	18	US-09-840-009-18	Sequence 18, Appl
11	83	92.2	18	US-09-840-009-22	Sequence 22, Appl
12	83	92.2	18	US-09-840-009-25	Sequence 25, Appl
13	83	92.2	18	US-09-840-009-29	Sequence 29, Appl
14	82	91.1	18	US-09-840-009-5	Sequence 5, Appl
15	82	91.1	18	US-09-840-009-12	Sequence 12, Appl
16	82	91.1	18	US-09-840-009-19	Sequence 19, Appl
17	82	91.1	18	US-09-840-009-26	Sequence 26, Appl
18	81	90.0	18	US-09-840-009-6	Sequence 6, Appl
19	81	90.0	18	US-09-840-009-13	Sequence 13, Appl
20	81	90.0	18	US-09-840-009-20	Sequence 20, Appl
21	81	90.0	18	US-09-840-009-14	Sequence 14, Appl
22	81	90.0	18	US-09-840-009-21	Sequence 21, Appl
23	81	90.0	18	US-09-840-009-27	Sequence 27, Appl
24	81	90.0	18	US-09-840-009-28	Sequence 28, Appl
25	81	90.0	18	US-09-840-009-3	Sequence 3, Appl
26	80	88.9	18	US-09-840-009-3	Sequence 10, Appl
27	80	88.9	18	US-09-840-009-3	Sequence 10, Appl

28	80	88.9	18	US-09-840-009-17	Sequence 17, Appl
29	80	88.9	18	US-09-840-009-24	Sequence 24, Appl
30	80	88.9	18	US-09-840-009-31	Sequence 31, Appl
31	74	82.2	18	US-09-840-009-34	Sequence 34, Appl
32	74	82.2	18	US-09-840-009-35	Sequence 35, Appl
33	72	80.0	18	US-09-840-009-32	Sequence 32, Appl
34	72	80.0	18	US-09-840-009-33	Sequence 33, Appl
35	68	75.6	18	US-09-840-009-1	Sequence 1, Appl
36	63	70.0	18	US-09-840-009-35	Sequence 36, Appl
37	63	70.0	18	US-09-840-009-37	Sequence 37, Appl
38	55	61.1	160	US-09-917-340-36	Sequence 36, Appl
39	52	57.8	169	US-09-270-767-35406	Sequence 37, Appl
40	52	57.8	169	US-09-270-767-35406	Sequence 36, Appl
41	48	53.3	205	US-09-134-001C-4766	Sequence 50623, A
42	44	48.9	24	US-09-785-059B-5	Sequence 4766, Ap
43	44	48.9	36	US-09-785-059B-6	Sequence 5, Appl
44	44	48.9	42	US-09-785-059B-7	Sequence 6, Appl
45	44	48.9	48	US-09-785-059B-8	Sequence 7, Appl
			4	US-09-785-059B-8	Sequence 8, Appl

ALIGNMENTS

RESULT 1
US-09-840-009-2

Sequence 2, Application US/09840009
Patent No. 6492328

GENERAL INFORMATION:

APPLICANT: Lehner, Robert I.

APPLICANT: Tack, Brian F.

TITLE OF INVENTION: NOVISPIRINS: ANTIMICROBIAL PEPTIDES

FILE REFERENCE: 06510-1950

CURRENT APPLICATION NUMBER: US/09/840,009

CURRENT FILING DATE: 2001-04-19

PRIOR APPLICATION NUMBER: US 09/606,858

PRIOR FILING DATE: 2000-06-28

NUMBER OF SEQ ID NOS: 37

SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 2

LENGTH: 18

TYPE: PRT

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: Synthetic antimicrobial peptide

US-09-840-009-2

Query Match

Best Local Similarity 97.8%; Score 88; DB 4; Length 18;

Matches 17; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Db 1 KNIRRIIRKIHIIKKYG 18

RESULT 2

US-09-840-009-9

Sequence 9, Application US/09840009

Patent No. 6492328

GENERAL INFORMATION:

APPLICANT: Lehner, Robert I.

APPLICANT: Tack, Brian F.

TITLE OF INVENTION: NOVISPIRINS: ANTIMICROBIAL PEPTIDES

FILE REFERENCE: 06510-1950

CURRENT APPLICATION NUMBER: US/09/840,009

CURRENT FILING DATE: 2001-04-19

PRIOR APPLICATION NUMBER: US 09/606,858

PRIOR FILING DATE: 2000-06-28

NUMBER OF SEQ ID NOS: 37

SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 9

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OM protein - protein search, using sw model

Run on: May 4, 2005, 13:00:51; Search time 93.3333 Seconds
(without alignments)
98.758 Million cell updates/sec

Title: US-09-642-744D-6
Perfect score: 90
Sequence: 1 KNIRRIIRKIRIKYK 18

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database: UniProt_02:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	55	61.1	160	1	SCS1_SHEEP
2	55	61.1	160	1	P49928 ovis aries
3	52	57.8	146	2	SCS2_SHEEP
4	49	54.4	2017	2	O9A1H3
5	48.5	53.9	314	2	O675T1
6	48.5	53.9	324	2	O651T6
7	48	53.3	235	2	O62X75
8	48	53.3	235	2	O9LJW2
9	47	52.2	232	1	TF3B_SCHPO
10	47	52.2	232	2	O7MT01
11	47	52.2	581	2	O6EBB6
12	46	51.1	3267	2	O81B20
13	46	51.1	93	2	O64D16
14	46	51.1	113	2	O70320
15	46	51.1	250	2	O6L7F9
16	46	51.1	282	2	O8DVR3
17	46	51.1	282	2	O8E4C0
18	46	51.1	319	2	O05804
19	46	51.1	343	2	O76CZ2
20	46	51.1	807	1	H1S8_PHOHL
21	46	51.1	1774	2	O754D8
22	45.5	50.6	2084	2	O81LJ6
23	45.5	50.6	208	1	TRPF_NEIMA
24	45.5	50.0	192	2	O896E1
25	45	50.0	192	2	O896E1
26	45	50.0	234	2	O59264
27	45	50.0	308	2	O8R2C7
28	45	50.0	420	1	PRIL_HUMAN
29	45	50.0	609	2	O72W21
30	45	50.0	647	2	O8F908
31	45	50.0	647	2	O62647
32	45	50.0	834	2	O7RRI0

32	45	50.0	1160	2	O81M12	O81m12 plasmodium
33	45	50.0	1634	2	DPOL_METYA	O86295 methanococc
34	44	48.9	78	2	O82YK7	O82YK7 pyrobaculum
35	44	48.9	93	1	V435_METYA	O57877 methanococc
36	44	48.9	124	2	O649W3	O649W3 uncultured
37	44	48.9	125	2	O64EA5	O64EA5 uncultured
38	44	48.9	165	2	O81B86	O81B86 plasmodium
39	44	48.9	231	2	O8R4G4	O8R4G4 thermoaer
40	44	48.9	233	2	O9L7X2	O9L7X2 clostridium
41	44	48.9	291	2	O8XJ18	O8XJ18 clostridium
42	44	48.9	301	2	O738Z6	O738Z6 bacillus ce
43	44	48.9	301	2	O6H2B4	O6H2B4 bacillus an
44	44	48.9	301	2	O63BX5	O63BX5 bacillus ce
45	44	48.9	301	2	O81E24	O81E24 bacillus ce

ALIGNMENTS

RESULT 1
SCS1_SHEEP
ID -SCS1_SHEEP STANDARD; PRT; 160 AA.
AC P49928;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Cathelin-related peptide SCS precursor 1 (Antibacterial peptide SWAP-29)
DE 29) (Myeloid antibacterial peptide SWAP-29).
OS Ovis aries (Sheep).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Caprinae; Ovis.
OX NCBI_Taxid:9940;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Bone marrow;
RA MEDLINE=96140581; PubMed=8549789; DOI=10.1016/0014-5793(95)01390-3;
RT Mahoney M.M., Lee A.Y., Brezinski-Caligiuri D.J., Huttner K.M.;
RT "Molecular analysis of the sheep cathelin family reveals a novel
RL antimicrobial peptide.";
RL PNAS Lett. 377:519-522(1995).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RA Huttner K.M., Mahoney M.M.;
RT Submitted (JUN-1996) to the EMBL/GenBank/DBJ databases.
RT -1- FUNCTION: Thermolabile, broad spectrum, bactericidal agent.
RT -1- SUBCELLULAR LOCATION: Secreted.
CC -1- SIMILARITY: Belongs to the cathelicidin family.

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EMBL: X92757; CA63412.1; -
EMBL: U60600; AAB49715.1; -
PDB: 1FRY; NMR: A=132-160.
InterPro: IPR001894; Cathelicidin.
Pfam: PF00666; Cathelicidins; 1.
ProDom: PD001838; Cathelicidins; 1.
PROSITE: PS00946; CATHELICIDIN; 1.
PROSITE: PS00947; CATHELICIDIN_2; 1.
3D-structure: Antibiotic; Pyroliidone carboxylic acid; Signal.
FT SIGNAL 1 29
FT PROPEP 30 131
FT PEPTIDE 132 160
FT MOD_RES 30 30
FT DISULFID 86 97
By similarity.
Cathelin-related peptide SCS.
Pyroliidone carboxylic acid (By similarity).
By similarity.

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OM protein - protein search, using sw model

Run on: May 4, 2005, 13:01:37 ; Search time 19 Seconds
(without alignments)
91.153 Million cell updates/sec

Title: US-09-642-744D-6
Perfect score: 90
Sequence: 1 KNIRRIIRKIHIIKKYG 18

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 791.*

1: p1r1:*
2: p1r2:*
3: p1r3:*
4: p1r4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	55	61.1	152	2	S68411 cathelin-related p
2	55	61.1	160	2	S68412 cathelin-related p
3	55	61.1	160	2	S68428 myeloid antimicrob
4	46	51.1	319	1	S19248 RNA-directed DNA p
5	45.5	50.6	208	2	G81169 N-(5'-phosphoribos
6	45.5	50.6	208	2	E81935 probable phosphori
7	45	50.0	234	2	D97108 DNA-dependent RNA
8	45	50.0	234	2	I40822 sigk protein - C10
9	45	50.0	420	2	S45630 DNA primase chain
10	45	50.0	1634	2	E64410 DNA-directed DNA p
11	44	48.9	96	2	C64354 hypothetical prote
12	44	48.9	483	2	S75359 hypothetical prote
13	44	48.9	540	2	T33982 hypothetical prote
14	44	48.9	1670	2	T06754 DNA-directed RNA p
15	43.5	48.3	381	1	C64416 conserved hypotet
16	43	47.8	210	2	AC1577 precortin isomeras
17	43	47.8	417	2	A33269 DNA primase (EC 2.
18	43	47.8	867	2	G69485 DNA-directed RNA p
19	43	47.8	1524	2	G84721 hypothetical prote
20	42	46.7	125	2	A99114 hypothetical prote
21	42	46.7	146	2	D90581 conserved hypotet
22	42	46.7	168	2	T08831 conserved hypotet
23	42	46.7	186	2	B90116 hypothetical prote
24	42	46.7	406	2	A71965 hypothetical prote
25	42	46.7	537	2	C90389 conserved hypotet
26	42	46.7	698	2	D64084 helicas (EC 3.6.1
27	42	46.7	849	2	A96592 hypothetical prote
28	41.5	46.1	483	2	B82160 hypothetical prote
29	41	45.6	108	2	C64490 hypothetical prote

30	41	45.6	117	2	T12722 hypothetical prote
31	41	45.6	152	2	A72385 arginine repressor
32	41	45.6	162	1	A53484 interleukin-15 pre
33	41	45.6	190	2	UC4514 TADA-binding prote
34	41	45.6	190	2	A85360 hypothetical prote
35	41	45.6	256	2	A35340 H+-transporting tw
36	41	45.6	277	2	A70158 ABC transporter, A
37	41	45.6	297	2	H70446 UTP-glucose-1-phos
38	41	45.6	337	2	S46010 hypothetical prote
39	41	45.6	358	2	B64309 hypothetical prote
40	41	45.6	507	2	T10753 intestinal DNA rep
41	41	45.6	613	2	F64056 probable ATP-depen
42	41	45.6	686	1	S28050 transforming prote
43	41	45.6	700	1	S01991 transforming prote
44	41	45.6	704	1	S33704 transforming prote
45	41	45.6	821	2	B71229 pyruvate, water di

ALIGNMENTS

RESULT 1
S68411
cathelin-related protein 2 precursor - sheep (fragment)
C/Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)
C/Date: 28-Oct-1996 #sequence_revision 13-Mar-1997 #text_change 21-Jan-2000
C/Accession: S68411
R/Mahoney, M.M.; Lee, A.Y.; Brezinski-Caliguri, D.J.; Huttner, K.M.
FEBS Lett. 377, 519-522, 1995
A/Title: Molecular analysis of the sheep cathelin family reveals a novel antimicrobial I
A/Reference number: S68411; MUID:96140581; PMID:8549789
A/Accession: S68411
A/Status: preliminary
A/Molecule type: mRNA
A/Residues: 1-152 <MAH>
A/Cross-references: EMBL:X92757
C/Genetics:
A/Genes: SC5-2
C/Superfamily: cathelin; cystatin homology
F/1-21/Domain: signal sequence #status predicted <SIG>
F/14-123/Domain: cystatin homology <CVS>
F/21-123/Domain: propeptide #status predicted <PRO>
F/124-152/Product: cathelin-related protein 2 #status predicted <MAT>
Query Match 61.1%; Score 55; DB 2; Length 152;
Best Local Similarity 55.6%; Pred. No. 0.37;
Matches 10; Conservative 4; Mismatches 4; Indels 0; Gaps 0;
OY 1 KNIRRIIRKIHIIKKYG 18
DB 124 RGLRRLGKRIAHGVKKYG 141
RESULT 2
S68412
cathelin-related protein 1 precursor - sheep
C/Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)
C/Date: 28-Oct-1996 #sequence_revision 13-Mar-1997 #text_change 21-Jan-2000
C/Accession: S68412
R/Mahoney, M.M.; Lee, A.Y.; Brezinski-Caliguri, D.J.; Huttner, K.M.
FEBS Lett. 377, 519-522, 1995
A/Title: Molecular analysis of the sheep cathelin family reveals a novel antimicrobial I
A/Reference number: S68411; MUID:96140581; PMID:8549789
A/Accession: S68412
A/Status: preliminary
A/Molecule type: mRNA
A/Residues: 1-160 <MAH>
A/Cross-references: EMBL:X92758
C/Genetics:
A/Genes: SC5-1
C/Superfamily: cathelin; cystatin homology
F/1-29/Domain: signal sequence #status predicted <SIG>
F/22-130/Domain: cystatin homology <CVS>

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OM protein - protein search, using sw model

Run on: May 4, 2005, 13:14:52 ; Search time 75 Seconds
(without alignments)
79.945 Million cell updates/sec

Title: US-09-642-744d-6

Sequence: 1 KNIRRIIRKIHIIKKYG 18

Scoring table:

BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1426032 seqs, 333106140 residues

Total number of hits satisfying chosen parameters: 1426032

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

- 1: /cgn2_6/ptodata/1/pubppa/US07_PUBCOMB.pep.*
- 2: /cgn2_6/ptodata/1/pubppa/PCT_NEW_PUB.pep.*
- 3: /cgn2_6/ptodata/1/pubppa/US06_NEW_PUB.pep.*
- 4: /cgn2_6/ptodata/1/pubppa/US06_PUBCOMB.pep.*
- 5: /cgn2_6/ptodata/1/pubppa/US07_NEW_PUB.pep.*
- 6: /cgn2_6/ptodata/1/pubppa/PCTUS_PUBCOMB.pep.*
- 7: /cgn2_6/ptodata/1/pubppa/US08_NEW_PUB.pep.*
- 8: /cgn2_6/ptodata/1/pubppa/US08_PUBCOMB.pep.*
- 9: /cgn2_6/ptodata/1/pubppa/US09_PUBCOMB.pep.*
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- 13: /cgn2_6/ptodata/1/pubppa/US10_PUBCOMB.pep.*
- 14: /cgn2_6/ptodata/1/pubppa/US10_PUBCOMB.pep.*
- 15: /cgn2_6/ptodata/1/pubppa/US10_PUBCOMB.pep.*
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- 17: /cgn2_6/ptodata/1/pubppa/US10_NEW_PUB.pep.*
- 18: /cgn2_6/ptodata/1/pubppa/US11_NEW_PUB.pep.*
- 19: /cgn2_6/ptodata/1/pubppa/US60_NEW_PUB.pep.*
- 20: /cgn2_6/ptodata/1/pubppa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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4	90	100.0	18	15	US-10-721-839-11
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6	88	97.8	18	9	US-09-840-009-9
7	88	97.8	18	9	US-09-840-009-16
8	88	97.8	18	9	US-09-840-009-23
9	88	97.8	18	9	US-09-840-009-30
10	88	97.8	18	14	US-10-060-102-9
11	88	97.8	18	14	US-10-060-102-12
12	88	97.8	18	15	US-10-721-839-9
13	88	97.8	18	15	US-10-721-839-12

14	88	97.8	29	14	US-10-060-102-8	Sequence 8, Appl1
15	88	97.8	29	15	US-10-721-839-8	Sequence 8, Appl1
16	83	92.2	18	9	US-09-840-009-8	Sequence 4, Appl1
17	83	92.2	18	9	US-09-840-009-11	Sequence 8, Appl1
18	83	92.2	18	9	US-09-840-009-11	Sequence 11, Appl1
19	83	92.2	18	9	US-09-840-009-15	Sequence 18, Appl1
20	83	92.2	18	9	US-09-840-009-18	Sequence 22, Appl1
21	83	92.2	18	9	US-09-840-009-22	Sequence 25, Appl1
22	83	92.2	18	9	US-09-840-009-25	Sequence 29, Appl1
23	83	92.2	18	9	US-09-840-009-25	Sequence 25, Appl1
24	83	92.2	18	14	US-10-060-102-25	Sequence 5, Appl1
25	83	92.2	18	15	US-10-721-839-25	Sequence 12, Appl1
26	82	91.1	18	9	US-09-840-009-5	Sequence 19, Appl1
27	82	91.1	18	9	US-09-840-009-12	Sequence 26, Appl1
28	82	91.1	18	9	US-09-840-009-15	Sequence 6, Appl1
29	82	91.1	18	9	US-09-840-009-26	Sequence 7, Appl1
30	81	90.0	18	9	US-09-840-009-6	Sequence 13, Appl1
31	81	90.0	18	9	US-09-840-009-7	Sequence 14, Appl1
32	81	90.0	18	9	US-09-840-009-13	Sequence 21, Appl1
33	81	90.0	18	9	US-09-840-009-14	Sequence 27, Appl1
34	81	90.0	18	9	US-09-840-009-20	Sequence 28, Appl1
35	81	90.0	18	9	US-09-840-009-21	Sequence 3, Appl1
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37	81	90.0	18	9	US-09-840-009-27	Sequence 17, Appl1
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40	80	88.9	18	9	US-09-840-009-10	Sequence 26, Appl1
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ALIGNMENTS

RESULT 1
US-10-060-102-10
Sequence 10, Application US/10060102
Publication No. US2003022829A1
GENERAL INFORMATION:
APPLICANT: MAURY, WENDY
APPLICANT: STAPLETON, JACK
APPLICANT: ROLLER, RICHARD
APPLICANT: STINSKI, MARK
APPLICANT: MCCRAY, PAUL B.
APPLICANT: TACK, BRIAN
TITLE OF INVENTION: NOVEL ANTIVIRAL ACTIVITIES OF PRIVATE THETA DEFENSINS AND MAMMAL.
FILE REFERENCE: IOWA.035US
CURRENT APPLICATION NUMBER: US/10/060,102
CURRENT FILING DATE: 2002-02-22
PRIOR APPLICATION NUMBER: 60/309,368
PRIOR FILING DATE: 2001-08-01
PRIOR APPLICATION NUMBER: 60/265,270
PRIOR FILING DATE: 2001-01-30
NUMBER OF SEQ ID NOS: 32
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 10
LENGTH: 18
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Synthetic
OTHER INFORMATION: Peptide
US-10-060-102-10

Query Match 100.0%; Score 90; DB 14; Length 18;
Best Local Similarity 100.0%; Pred. No. 4.3e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 KNIRRIIRKIHIIKKYG 18

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OM protein - protein search, using sw model

Run on: May 4, 2005, 13:02:32 ; Search time 25.6667 Seconds
(without alignments)
52.351 Million cell updates/sec

Title: US-09-642-744D-6

Perfect score: 90

Sequence: 1 KNIRRIIRKIHIKKYG 18

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents, AA.*
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2: /cgn2_6/ptodata/1/aa/5B.COMB.pep.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	ID	Description
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2	88	97.8	18 4 US-09-840-009-9	Sequence 9, Appli
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5	88	97.8	18 4 US-09-840-009-30	Sequence 23, Appli
6	83	92.2	18 4 US-09-840-009-4	Sequence 30, Appli
7	83	92.2	18 4 US-09-840-009-8	Sequence 4, Appli
8	83	92.2	18 4 US-09-840-009-11	Sequence 8, Appli
9	83	92.2	18 4 US-09-840-009-15	Sequence 11, Appli
10	83	92.2	18 4 US-09-840-009-18	Sequence 15, Appli
11	83	92.2	18 4 US-09-840-009-22	Sequence 18, Appli
12	83	92.2	18 4 US-09-840-009-25	Sequence 22, Appli
13	83	92.2	18 4 US-09-840-009-29	Sequence 25, Appli
14	82	91.1	18 4 US-09-840-009-3	Sequence 29, Appli
15	82	91.1	18 4 US-09-840-009-5	Sequence 3, Appli
16	82	91.1	18 4 US-09-840-009-12	Sequence 19, Appli
17	82	91.1	18 4 US-09-840-009-19	Sequence 12, Appli
18	81	90.0	18 4 US-09-840-009-26	Sequence 26, Appli
19	81	90.0	18 4 US-09-840-009-6	Sequence 6, Appli
20	81	90.0	18 4 US-09-840-009-7	Sequence 7, Appli
21	81	90.0	18 4 US-09-840-009-13	Sequence 13, Appli
22	81	90.0	18 4 US-09-840-009-14	Sequence 14, Appli
23	81	90.0	18 4 US-09-840-009-20	Sequence 20, Appli
24	81	90.0	18 4 US-09-840-009-21	Sequence 21, Appli
25	81	90.0	18 4 US-09-840-009-27	Sequence 27, Appli
26	80	88.9	18 4 US-09-840-009-28	Sequence 28, Appli
27	80	88.9	18 4 US-09-840-009-3	Sequence 3, Appli
27	80	88.9	18 4 US-09-840-009-10	Sequence 10, Appli

28	80	88.9	18 4 US-09-840-009-17	Sequence 17, Appli
29	80	88.9	18 4 US-09-840-009-24	Sequence 24, Appli
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32	74	82.2	18 4 US-09-840-009-35	Sequence 35, Appli
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34	72	80.0	18 4 US-09-840-009-33	Sequence 33, Appli
35	68	75.6	18 4 US-09-840-009-1	Sequence 1, Appli
36	63	70.0	18 4 US-09-840-009-36	Sequence 36, Appli
37	63	70.0	18 4 US-09-840-009-37	Sequence 37, Appli
38	55	61.1	160 4 US-09-917-340-36	Sequence 36, Appli
39	52	57.8	169 4 US-09-270-767-35406	Sequence 35406, A
40	52	57.8	169 4 US-09-270-767-50623	Sequence 50623, A
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45	44	48.9	48 4 US-09-785-059B-8	Sequence 8, Appli

ALIGNMENTS

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RESULT 1
US-09-840-009-2
Sequence 2, Application US/09840009
Patent No. 6492328
GENERAL INFORMATION:
APPLICANT: Lehrer, Robert I.
APPLICANT: Waring, Alan J.
APPLICANT: Tack, Brian F.
TITLE OF INVENTION: NOVISPIRINS: ANTIMICROBIAL PEPTIDES
FILE REFERENCE: 06510-195W0
CURRENT FILING DATE: 2001-04-19
PRIOR APPLICATION NUMBER: US/09/840,009
PRIOR FILING DATE: 2000-06-28
NUMBER OF SEQ ID NOS: 37
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 2
LENGTH: 18
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Synthetic antimicrobial peptide
US-09-840-009-2
Query Match          97.8%; Score 88; DB 4; Length 18;
Best Local Similarity 94.4%; Pred. NO. 3.9e-07;
Matches 17; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY      1 KNIRRIIRKIHIKKYG 18
Db      1 KNIRRIIRKIHIKKYG 18
RESULT 2
US-09-840-009-9
Sequence 9, Application US/09840009
Patent No. 6492328
GENERAL INFORMATION:
APPLICANT: Lehrer, Robert I.
APPLICANT: Waring, Alan J.
APPLICANT: Tack, Brian F.
TITLE OF INVENTION: NOVISPIRINS: ANTIMICROBIAL PEPTIDES
FILE REFERENCE: 06510-195W0
CURRENT FILING DATE: 2001-04-19
PRIOR APPLICATION NUMBER: US/09/840,009
PRIOR FILING DATE: 2000-06-28
NUMBER OF SEQ ID NOS: 37
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 9

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OM protein - protein search, using SW model

Run on: May 4, 2005, 12:52:41 ; Search time 101 Seconds

(without alignments)
68.928 Million cell updates/sec

Title: US-09-642-744D-6

Sequence: 1 KNIRRIKRIHIKKYG 18

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

1: Geneseqp16dec04:*
2: geneseqp19908:*
3: geneseqp20008:*
4: geneseqp20018:*
5: geneseqp20028:*
6: geneseqp20038:*
7: geneseqp20038:*
8: geneseqp20048:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	90	100.0	18	4	AAE20871
2	90	100.0	18	5	AAE20878
3	90	100.0	18	5	AAE20857
4	90	100.0	20	4	AAE20872
5	88	97.8	18	4	AAE20858
6	88	97.8	18	4	AAE20865
7	88	97.8	18	4	AAE20868
8	88	97.8	18	5	AAE20875
9	88	97.8	18	5	AAE20882
10	88	97.8	18	5	AAE20854
11	88	97.8	18	5	AAE20861
12	88	97.8	18	5	AAE20868
13	88	97.8	18	5	AAE20876
14	88	97.8	18	5	AAE20879
15	88	97.8	29	4	AAE20875
16	88	97.8	29	4	AAE20875
17	88	97.8	18	5	AAE20870
18	88	97.8	18	5	AAE20860
19	88	97.8	18	5	AAE20881
20	88	97.8	18	5	AAE20867
21	88	97.8	18	5	AAE20874
22	88	97.8	18	5	AAE20863
23	88	97.8	18	5	AAE20877
24	88	97.8	18	5	AAE20856
25	88	97.8	18	5	AAE20892

ALIGNMENTS

26	82	91.1	18	5	AAE20871	AAE20871 S10-novis
27	82	91.1	18	5	AAE20878	AAE20878 S11-novis
28	82	91.1	18	5	AAE20857	AAE20857 S6-novisp
29	81	90.0	18	5	AAE20872	AAE20872 E10-novis
30	81	90.0	18	5	AAE20873	AAE20873 D10-novis
31	81	90.0	18	5	AAE20858	AAE20858 E6-novisp
32	81	90.0	18	5	AAE20865	AAE20865 D7-novisp
33	81	90.0	18	5	AAE20879	AAE20879 E11-novis
34	81	90.0	18	5	AAE20862	AAE20862 E7-novisp
35	81	90.0	18	5	AAE20880	AAE20880 D11-novis
36	81	90.0	18	5	AAE20885	AAE20885 D6-novisp
37	80	88.9	18	5	AAE20882	AAE20882 G7-novisp
38	80	88.9	18	5	AAE20876	AAE20876 G11-novis
39	80	88.9	18	5	AAE20883	AAE20883 G10-novis
40	80	88.9	18	5	AAE20889	AAE20889 G10-novis
41	80	88.9	18	5	AAE20855	AAE20855 G6-novisp
42	80	88.9	18	5	AAE20873	AAE20873 Synthetic
43	80	88.9	18	5	AAE20877	AAE20877 Synthetic
44	80	88.9	18	6	AAE20856	AAE20856 Antimicro
45	80	88.9	18	8	AAE20864	AAE20864 Novispirt

RESULT 1
ID AAB70654 standard; peptide, 18 AA.
AAB70654;

15-MAY-2001 (first entry)

Ovine SNAP 29 cathelicidin derived antimicrobial peptide SEQ ID NO.7.

Ovine, SNAP29, lupine, RCAP 18; cathelicidin; antimicrobial; bactericidal; antibiotic; antiviral; microbial growth inhibitor; proliferation inhibitor; gene therapy; Pseudomonas aeruginosa; Burkholderia cepacia; Alcaligenes; Xanthomonas.

Ovis aries.

WO200112668-A1.

22-FEB-2001.

18-AUG-2000; 2000WO-US022781.

18-AUG-1999; 99US-0149866P.

(IOWA) UNIV IOWA RES FOUND.
(REGC) UNIV CALIFORNIA.

Tack BE, Mccray P, Welsh M, Travis SM, Lehrer R;
WPI; 2001-234911/24.

New antimicrobial peptides useful as antibiotics for inhibiting growth and proliferation of microbes, and for treating microbial infections.

Claim 1; Page 103; 137pp; English.

AAE20871 to AAB70675 represent antimicrobial peptides (1), of which SNAP 29 cathelicidin family peptide, and AAB70675 are derived from the lupine RCAP 18 cathelicidin family peptide. (1) have antimicrobial and antiviral activities, and can be used as antibiotic, growth and proliferation inhibitors and in gene therapy. (1) are useful for inhibiting microbial growth in an environment capable of sustaining such growth, for inhibiting microbial growth or strain in a host, and inhibiting the growth of drug-resistant microbial strains such as Pseudomonas aeruginosa, Burkholderia cepacia, Alcaligenes and Xanthomonas

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OM protein - protein search, using sw model

Run on: May 4, 2005, 13:00:51 / Search time 93.333 Seconds
(without alignments)
98.758 Million cell updates/sec

Title: US-09-642-744D-1

Perfect score: 90
Sequence: 1 KNLRIRIKRIHKKYG 18

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database: UniProt 03: *
1: uniprot_eprc: *
2: uniprot_trembl: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	57	63.3	160	1 SC51_SHEEP	P49928 ovis aries
2	57	63.3	160	1 SC52_SHEEP	P49929 ovis aries
3	54	60.0	146	2 O9A1H3	O9A1H3 carsonella
4	50	55.6	255	2 O9LJW2	O9LJW2 arabidopsis
5	49	54.4	581	2 O6EBB6	O6EBB6 campylobact
6	48	53.3	250	2 O6LFF9	O6LFF9 plasmodium
7	48	53.3	500	1 TP3B_SCHPO	O9P670 echinosacch
8	48	53.3	3267	2 O8IBZ0	O8IBZ0 plasmodium
9	47	52.2	113	2 O703Z0	O703Z0 thermoprote
10	47	52.2	2017	2 O675T1	O675T1 okopileura
11	46.5	51.7	314	2 O62X75	O62X75 bacillus th
12	46.5	51.7	322	2 O62X75	O62X75 bacillus th
13	46	51.1	282	2 O8DYR3	O8DYR3 streptococc
14	46	51.1	282	2 O8DYR3	O8DYR3 streptococc
15	46	51.1	319	2 O05804	O05804 escherichia
16	46	51.1	349	2 O736D5	O736D5 bacillus ce
17	46	51.1	349	2 O81P89	O81P89 bacillus an
18	46	51.1	349	2 O6H1T2	O6H1T2 bacillus th
19	46	51.1	684	2 O7QNN1	O7QNN1 giardia lam
20	46	51.1	954	2 O9GQI5	O9GQI5 giardia lam
21	46	51.1	969	2 O9J022	O9J022 giardia lam
22	45.5	50.6	381	1 TH11_METUA	O58341 methanococc
23	45	50.0	232	2 O7WMT0	O7WMT0 plasmodium
24	45	50.0	308	2 O8R2C7	O8R2C7 porphyromon
25	45	50.0	402	2 O8R2C7	O8R2C7 mus musculu
26	45	50.0	834	2 O7RR10	O7RR10 plasmodium
27	45	50.0	1634	1 DPOL_METUA	O58295 methanococc
28	44	48.9	78	2 O82YK7	O82YK7 pyrobaculum
29	44	48.9	93	2 O64DI6	O64DI6 uncultured
30	44	48.9	124	2 O649W3	O649W3 uncultured
31	44	48.9	125	2 O64EAS	O64EAS uncultured

ALIGNMENTS

RESULT 1	ID	SC51_SHEEP	STANDARD	PRT	160 AA
AC	P49928;				
DT	01-OCT-1996 (Rel. 34, Created)				
DT	01-OCT-1996 (Rel. 34, Last sequence update)				
DT	25-OCT-2004 (Rel. 45, Last annotation update)				
DE	Cathelin-related peptide SCS precursor 1 (Antibacterial peptide SWAP-29).				
DE	29) (Myeloid antibacterial peptide SWAP-29).				
OS	Ovis aries (Sheep).				
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;				
OX	NCBI_TaxID=99940;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RX	TISSUE=Bone marrow;				
RX	MEDLINE=96140581; PubMed=8549789; DOI=10.1016/0014-5793(95)01390-3;				
RA	Mahoney M.M., Lee A.Y., Brezinski-Caliguri D.J., Hutner K.M.;				
RT	"Molecular analysis of the sheep cathelin family reveals a novel				
RT	antimicrobial peptide."				
RL	FEBS Lett. 377:519-522(1995).				
RN	[2]				
RP	SEQUENCE FROM N.A.				
RC	TISSUE=Liver;				
RA	Hutner K.M., Mahoney M.M.;				
RL	Submitted (JUN-1996) to the EMBL/GenBank/DBJ databases.				
CC	-1- FUNCTION: Thermostable, broad spectrum, bactericidal agent.				
CC	-1- SUBCELLULAR LOCATION: Secreted.				
CC	-1- SIMILARITY: Belongs to the cathelicidin family.				
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration				
CC	between the Swiss Institute of Bioinformatics and the EMBL outstation -				
CC	the European Bioinformatics Institute. There are no restrictions on its				
CC	use by non-profit institutions as long as its content is in no way				
CC	modified and this statement is not removed. Usage by and for commercial				
CC	entities requires a license agreement (See http://www.isb-sib.ch/announce/				
CC	or send an email to license@sib-sib.ch).				
DR	EMBL; X52757; CAA63412.1; -				
DR	EMBL; U60600; AAB49715.1; -				
DR	PDB; 1FRY; NMR; A=132-160.				
DR	InterPro; IPR001894; Cathelicidin.				
DR	Pfam; PF00666; Cathelicidin; 1.				
DR	ProDom; PD001838; Cathelicidin; 1.				
DR	PROSITE; PS00946; CATHEDICIDINS 1; 1.				
DR	PROSITE; PS00947; CATHEDICIDINS 2; 1.				
KW	3D-structure; Antibiotic; Pyroglutamate carboxylic acid; Signal.				
FT	SIGNAL	1	29		
FT	PROPEP	30	131		
FT	PEPTIDE	132	160		
FT	MOD_RES	30	30		
FT	DISULFID	86	97		

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OM protein - protein search, using sw model

Run on: May 4, 2005, 13:01:37 ; Search time 19 Seconds
(without alignments)
91.153 Million cell updates/sec

Title: US-09-642-744D-1

Sequence: 1 KNLRRIRKIHIIKKYG 18

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 segs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 79:*
1: p1r1:*
2: p1r2:*
3: p1r3:*
4: p1r4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	57	63.3	152	2	S68411 cathelin-related p
2	57	63.3	160	2	S68412 cathelin-related p
3	57	63.3	160	2	S68228 myeloid antimicrob
4	46	51.1	319	1	S19248 RNA-directed DNA p
5	45.5	50.6	381	1	C64416 conserved hypotet
6	45	50.0	1634	2	E64410 DNA-directed RNA p
7	44	48.9	1670	2	T06754 DNA-directed RNA p
8	43.5	48.3	208	2	G81169 N-(5'-phosphoribos
9	43.5	48.3	208	2	B81935 probable phosphori
10	43	47.8	210	2	AC1577 precorrin isomeras
11	43	47.8	234	2	D97108 DNA-dependent RNA
12	43	47.8	234	2	I40822 sigk protein - C10
13	43	47.8	420	2	S45630 DNA primase chain
14	43	47.8	537	2	C90389 conserved hypotet
15	42	46.7	41	2	S77368 hypothetical prote
16	42	46.7	96	2	C64354 hypothetical prote
17	42	46.7	125	2	A99114 hypothetical prote
18	42	46.7	146	2	D90581 hypothetical prote
19	42	46.7	152	2	A72385 conserved hypotet
20	42	46.7	168	2	T08831 arginine repressor
21	42	46.7	186	2	B90116 disease resistance
22	42	46.7	187	2	H71819 hypothetical prote
23	42	46.7	359	2	S77322 hypothetical prote
24	42	46.7	429	2	D90428 hypothetical prote
25	42	46.7	483	2	S75369 hypothetical prote
26	42	46.7	507	2	T10753 intestinal DNA rep
27	42	46.7	540	2	T33982 hypothetical prote
28	42	46.7	594	2	D70127 alanine-tRNA ligas
29	42	46.7	698	2	D64084 helicase (EC 3.6.1

30	42	46.7	937	2	T37241	olfactory channel
31	42	46.7	957	2	D88651	protein B012.5 (i
32	42	46.7	1741	2	T15978	hypothetical prote
33	41.5	46.1	313	2	A89971	cmp-binding-factor
34	41	45.6	117	2	T12722	hypothetical prote
35	41	45.6	181	2	B90246	TATA box binding p
36	41	45.6	190	2	A85360	hypothetical prote
37	41	45.6	198	2	S55311	hypothetical prote
38	41	45.6	207	2	E70407	TATA-binding prote
39	41	45.6	256	2	A35340	probable CDP-alcoh
40	41	45.6	297	2	H70446	H+-transporting tw
41	41	45.6	337	2	S46010	urp-glucose-1-phos
42	41	45.6	338	2	D90017	hypothetical prote
43	41	45.6	367	2	S19172	hypothetical prote
44	41	45.6	414	2	G64091	cytochrome P450 2B
45	41	45.6	417	2	A33269	cell division prot
						DNA primase (EC 2.

ALIGNMENTS

RESULT 1
S68411
C:Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)
C>Date: 28-Oct-1996 #sequence_revision 13-Mar-1997 #text_change 21-Jan-2000
C:Accession: S68411
R:Mahoney, M.M.; Lee, A.Y.; Brezinski-Caliguri, D.J.; Huttner, K.M.
F:14-122/Domain: signal sequence #status predicted <SIG>
A:Reference number: S68411; MUID:96140581; PMID:8549789
A:Accession: S68411
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-152 <MAH>
A:Cross-references: EMBL:X92757
C:Gene: SCS-2
C:Superfamily: cathelin; cystatin homology
F:1-21/Domain: signal sequence #status predicted <SIG>
F:14-122/Domain: cystatin homology <CYS>
F:21-123/Domain: propeptide #status predicted <PRO>
F:124-152/Product: cathelin-related protein 2 #status predicted <MAT>

Query Match 63.3%; Score 57; DB 2; Length 152;
Best Local Similarity 61.1%; Pred. No. 0.21;
Matches 11; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 KNLRRIRKIHIIKKYG 18
DB 124 RGLRLRGKIHAGVKKYG 141

RESULT 2
S68412
C:Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)
C>Date: 28-Oct-1996 #sequence_revision 13-Mar-1997 #text_change 21-Jan-2000
C:Accession: S68412
R:Mahoney, M.M.; Lee, A.Y.; Brezinski-Caliguri, D.J.; Huttner, K.M.
F:14-122/Domain: signal sequence #status predicted <SIG>
A:Reference number: S68411; MUID:96140581; PMID:8549789
A:Accession: S68412
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-160 <MAH>
A:Cross-references: EMBL:X92758
C:Gene: SCS-1
C:Superfamily: cathelin; cystatin homology
F:1-29/Domain: signal sequence #status predicted <SIG>
F:122-130/Domain: cystatin homology <CYS>

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OM protein - protein search, using sw model

Run on: May 4, 2005, 13:14:52 / Search time 75 Seconds
(without alignments)
79.945 Million cell updates/sec

Title: US-09-642-744D-1

Perfect score: 1 KMLRRIIRKIIHIKYG 18

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 1426032 seqs, 333106140 residues

Total number of hits satisfying chosen parameters: 1426032

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database:

Published Applications AA:*

- 1: /cgn2_6/ptodata/1/pubppaa/US07_PUBCOMB.pep.*
- 2: /cgn2_6/ptodata/1/pubppaa/PCF_NEW_PUB.pep.*
- 3: /cgn2_6/ptodata/1/pubppaa/US06_NEW_PUB.pep.*
- 4: /cgn2_6/ptodata/1/pubppaa/US06_PUBCOMB.pep.*
- 5: /cgn2_6/ptodata/1/pubppaa/US07_PUB.pep.*
- 6: /cgn2_6/ptodata/1/pubppaa/US07_PUBCOMB.pep.*
- 7: /cgn2_6/ptodata/1/pubppaa/US08_PUB.pep.*
- 8: /cgn2_6/ptodata/1/pubppaa/US08_PUBCOMB.pep.*
- 9: /cgn2_6/ptodata/1/pubppaa/US09_PUBCOMB.pep.*
- 10: /cgn2_6/ptodata/1/pubppaa/US09_PUBCOMB.pep.*
- 11: /cgn2_6/ptodata/1/pubppaa/US09_PUBCOMB.pep.*
- 12: /cgn2_6/ptodata/1/pubppaa/US09_PUB.pep.*
- 13: /cgn2_6/ptodata/1/pubppaa/US10_PUBCOMB.pep.*
- 14: /cgn2_6/ptodata/1/pubppaa/US10_PUBCOMB.pep.*
- 15: /cgn2_6/ptodata/1/pubppaa/US10_PUBCOMB.pep.*
- 16: /cgn2_6/ptodata/1/pubppaa/US10_PUBCOMB.pep.*
- 17: /cgn2_6/ptodata/1/pubppaa/US10_PUBCOMB.pep.*
- 18: /cgn2_6/ptodata/1/pubppaa/US10_PUB.pep.*
- 19: /cgn2_6/ptodata/1/pubppaa/US60_NEW_PUB.pep.*
- 20: /cgn2_6/ptodata/1/pubppaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	90	100.0	18	9	US-09-840-009-2
2	90	100.0	18	9	US-09-840-009-9
3	90	100.0	18	9	US-09-840-009-16
4	90	100.0	18	9	US-09-840-009-23
5	90	100.0	18	9	US-09-840-009-30
6	90	100.0	18	14	US-10-060-102-9
7	90	100.0	18	14	US-10-060-102-12
8	90	100.0	18	15	US-10-721-839-9
9	90	100.0	18	15	US-10-721-839-12
10	90	100.0	29	14	US-10-060-102-8
11	90	100.0	29	15	US-10-721-839-8
12	88	97.8	18	14	US-10-060-102-10
13	88	97.8	18	14	US-10-060-102-11

14	88	97.8	18	15	US-10-721-839-10	Sequence 10, Appl
15	88	97.8	18	15	US-10-721-839-11	Sequence 11, Appl
16	85	94.4	18	9	US-09-840-009-4	Sequence 4, Appl
17	85	94.4	18	9	US-09-840-009-8	Sequence 8, Appl
18	85	94.4	18	9	US-09-840-009-11	Sequence 11, Appl
19	85	94.4	18	9	US-09-840-009-15	Sequence 15, Appl
20	85	94.4	18	9	US-09-840-009-18	Sequence 18, Appl
21	85	94.4	18	9	US-09-840-009-22	Sequence 22, Appl
22	85	94.4	18	9	US-09-840-009-25	Sequence 25, Appl
23	85	94.4	18	9	US-09-840-009-29	Sequence 29, Appl
24	85	94.4	18	14	US-10-060-102-25	Sequence 25, Appl
25	85	94.4	18	15	US-10-721-839-25	Sequence 25, Appl
26	84	93.3	18	9	US-09-840-009-5	Sequence 5, Appl
27	84	93.3	18	9	US-09-840-009-12	Sequence 12, Appl
28	84	93.3	18	9	US-09-840-009-19	Sequence 19, Appl
29	84	93.3	18	9	US-09-840-009-26	Sequence 26, Appl
30	83	92.2	18	9	US-09-840-009-6	Sequence 6, Appl
31	83	92.2	18	9	US-09-840-009-7	Sequence 7, Appl
32	83	92.2	18	9	US-09-840-009-13	Sequence 13, Appl
33	83	92.2	18	9	US-09-840-009-14	Sequence 14, Appl
34	83	92.2	18	9	US-09-840-009-20	Sequence 20, Appl
35	83	92.2	18	9	US-09-840-009-21	Sequence 21, Appl
36	83	92.2	18	9	US-09-840-009-27	Sequence 27, Appl
37	83	92.2	18	9	US-09-840-009-28	Sequence 28, Appl
38	82	91.1	18	9	US-09-840-009-3	Sequence 3, Appl
39	82	91.1	18	9	US-09-840-009-10	Sequence 10, Appl
40	82	91.1	18	9	US-09-840-009-17	Sequence 17, Appl
41	82	91.1	18	9	US-09-840-009-24	Sequence 24, Appl
42	82	91.1	18	9	US-09-840-009-31	Sequence 31, Appl
43	82	91.1	18	14	US-10-060-102-26	Sequence 26, Appl
44	82	91.1	18	14	US-10-077-624-17	Sequence 17, Appl
45	82	91.1	18	15	US-10-721-839-26	Sequence 26, Appl

ALIGNMENTS

RESULT 1
US-09-840-009-2
Sequence 2, Application US/09840009
Patent No. US20020082195A1
GENERAL INFORMATION:
APPLICANT: Lehre, Robert I.
APPLICANT: Waring, Alan J.
TITLE OF INVENTION: NOVEL PEPTIDES
FILE REFERENCE: 06510-195WO
CURRENT APPLICATION NUMBER: US/09/840, 009
CURRENT FILING DATE: 2001-04-19
PRIOR APPLICATION NUMBER: US 09/606, 858
PRIOR FILING DATE: 2000-06-28
NUMBER OF SEQ ID NOS: 37
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 2
LENGTH: 18
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Synthetic antimicrobial peptide
US-09-840-009-2

Query Match 100.0%; Score 90; DB 9; Length 18;
Best Local Similarity 100.0%; Pred. No. 5.4e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KMLRRIIRKIIHIKYG 18
DB 1 KMLRRIIRKIIHIKYG 18

RESULT 2
US-09-840-009-9
Sequence 9, Application US/09840009

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: May 4, 2005, 13:02:32 ; Search time 25.6667 Seconds
(without alignments)
52.351 Million cell updates/sec

Title: US-09-642-744D-1
Perfect score: 90
Sequence: 1 KNLRRIIRKIHIKKYG 18

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA:*
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3: /cgn2_6/ptodata/1/1aa/6A.COMB.pep:*
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5: /cgn2_6/ptodata/1/1aa/PCTUS.COMB.pep:*
6: /cgn2_6/ptodata/1/1aa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	90	100.0	18	4	US-09-840-009-2
2	90	100.0	18	4	US-09-840-009-9
3	90	100.0	18	4	US-09-840-009-15
4	90	100.0	18	4	US-09-840-009-23
5	90	100.0	18	4	US-09-840-009-30
6	85	94.4	18	4	US-09-840-009-4
7	85	94.4	18	4	US-09-840-009-8
8	85	94.4	18	4	US-09-840-009-11
9	85	94.4	18	4	US-09-840-009-15
10	85	94.4	18	4	US-09-840-009-18
11	85	94.4	18	4	US-09-840-009-22
12	85	94.4	18	4	US-09-840-009-25
13	85	94.4	18	4	US-09-840-009-29
14	84	93.3	18	4	US-09-840-009-5
15	84	93.3	18	4	US-09-840-009-12
16	84	93.3	18	4	US-09-840-009-19
17	84	93.3	18	4	US-09-840-009-26
18	83	92.2	18	4	US-09-840-009-6
19	83	92.2	18	4	US-09-840-009-7
20	83	92.2	18	4	US-09-840-009-13
21	83	92.2	18	4	US-09-840-009-14
22	83	92.2	18	4	US-09-840-009-20
23	83	92.2	18	4	US-09-840-009-21
24	83	92.2	18	4	US-09-840-009-27
25	83	92.2	18	4	US-09-840-009-28
26	82	91.1	18	4	US-09-840-009-3
27	82	91.1	18	4	US-09-840-009-10

28	82	91.1	18	4	US-09-840-009-17	Sequence 17, Appl
29	82	91.1	18	4	US-09-840-009-24	Sequence 24, Appl
30	82	91.1	18	4	US-09-840-009-31	Sequence 31, Appl
31	76	84.4	18	4	US-09-840-009-34	Sequence 34, Appl
32	76	84.4	18	4	US-09-840-009-35	Sequence 35, Appl
33	74	82.2	18	4	US-09-840-009-32	Sequence 32, Appl
34	74	82.2	18	4	US-09-840-009-33	Sequence 33, Appl
35	70	77.8	18	4	US-09-840-009-1	Sequence 1, Appl
36	65	72.2	18	4	US-09-840-009-36	Sequence 36, Appl
37	65	72.2	18	4	US-09-840-009-37	Sequence 37, Appl
38	57	63.3	160	4	US-09-917-340-36	Sequence 37, Appl
39	50	55.6	169	4	US-09-270-767-35406	Sequence 36, Appl
40	50	55.6	169	4	US-09-270-767-50623	Sequence 35406, A
41	50	55.6	205	3	US-09-134-001C-4766	Sequence 4766, Ap
42	43.5	48.3	167	4	US-09-710-279-1502	Sequence 1502, Ap
43	43.5	48.3	320	3	US-09-134-001C-3823	Sequence 3823, Ap
44	43	47.8	823	4	US-09-949-016-8339	Sequence 8339, Ap
45	42	46.7	24	4	US-09-785-059B-5	Sequence 5, Appl

ALIGNMENTS

```

RESULT 1
US-09-840-009-2
; Sequence 2, Application US/09840009
; Patent No. 6492328
; GENERAL INFORMATION:
; APPLICANT: Lehner, Robert I.
; APPLICANT: Waring, Alan J.
; TITLE OF INVENTION: NOVISPIRINS: ANTIMICROBIAL PEPTIDES
; FILE REFERENCE: 06510-195WO
; CURRENT FILING DATE: 2001-04-19
; PRIOR APPLICATION NUMBER: US/09/840,009
; PRIOR FILING DATE: 2000-06-28
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic antimicrobial peptide
US-09-840-009-2
; Query Match      100.0%; Score 90; DB 4; Length 18;
; Best Local Similarity 100.0%; Pred. No. 2.1e-07;
; Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
;
Cy      1 KNLRRIIRKIHIKKYG 18
Db      1 KNLRRIIRKIHIKKYG 18

RESULT 2
US-09-840-009-9
; Sequence 9, Application US/09840009
; Patent No. 6492328
; GENERAL INFORMATION:
; APPLICANT: Lehner, Robert I.
; APPLICANT: Waring, Alan J.
; APPLICANT: Tack, Brian F.
; TITLE OF INVENTION: NOVISPIRINS: ANTIMICROBIAL PEPTIDES
; FILE REFERENCE: 06510-195WO
; CURRENT FILING DATE: 2001-04-19
; PRIOR APPLICATION NUMBER: US/09/840,009
; PRIOR FILING DATE: 2000-06-28
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 9

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: May 4, 2005, 12:52:41 ; Search time 101 Seconds
(without alignments)
68.928 Million cell updates/sec

Title: US-09-642-744d-1

Perfect score: 90

Sequence: 1 KMLRRIRKIHITKYG 18

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_16Dec04:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	90	100.0	18	4	AAB70655
2	90	100.0	18	4	AAB70648
3	90	100.0	18	5	AAE20882
4	90	100.0	18	5	AAE20875
5	90	100.0	18	5	AAE20861
6	90	100.0	18	5	AAE20854
7	90	100.0	18	5	AAE20868
8	90	100.0	18	5	ABP53276
9	90	100.0	18	5	ABP53279
10	90	100.0	29	4	AAE20875
11	90	100.0	29	5	ABP53275
12	88	97.8	18	4	AAE20854
13	88	97.8	18	5	ABP53278
14	88	97.8	18	5	ABP53277
15	88	97.8	20	4	AAE20870
16	85	94.4	18	5	AAE20860
17	85	94.4	18	5	AAE20881
18	85	94.4	18	5	AAE20867
19	85	94.4	18	5	AAE20874
20	85	94.4	18	5	AAE20873
21	85	94.4	18	5	AAE20863
22	85	94.4	18	5	AAE20877
23	85	94.4	18	5	AAE20856
24	85	94.4	18	5	ABP53292
25	84	93.3	18	5	AAE20864

26	84	93.3	18	5	AAE20871	AAE20871 S10-novis
27	84	93.3	18	5	AAE20878	AAE20878 S11-novis
28	84	93.3	18	5	AAE20857	AAE20857 S6-novisp
29	83	92.2	18	5	AAE20872	AAE20872 E10-novis
30	83	92.2	18	5	AAE20873	AAE20873 D10-novis
31	83	92.2	18	5	AAE20858	AAE20858 E6-novisp
32	83	92.2	18	5	AAE20866	AAE20866 D7-novisp
33	83	92.2	18	5	AAE20879	AAE20879 E11-novis
34	83	92.2	18	5	AAE20865	AAE20865 E7-novisp
35	83	92.2	18	5	AAE20880	AAE20880 D11-novis
36	83	92.2	18	5	AAE20859	AAE20859 D6-novisp
37	82	91.1	18	5	AAE20862	AAE20862 G7-novisp
38	82	91.1	18	5	AAE20876	AAE20876 G11-novis
39	82	91.1	18	5	AAE20883	AAE20883 G10-novis
40	82	91.1	18	5	AAE20869	AAE20869 G10-novis
41	82	91.1	18	5	AAE20855	AAE20855 G6-novisp
42	82	91.1	18	5	ABP53293	ABP53293 Synthetic
43	82	91.1	18	6	ABP72293	ABP72293 Antimicro
44	82	91.1	18	6	ADQ15520	ADQ15520 Antimicro
45	82	91.1	18	8	ADQ15575	ADQ15575 Novispirti

ALIGNMENTS

RESULT 1	
AAB70655	AAB70655 standard; peptide; 18 AA.
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AC	AAB70655;
XX	
DT	15-MAY-2001 (first entry)
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DE	Ovine SNAP 29 cathelicidin derived antimicrobial peptide SEQ ID NO:8.
XX	
KM	Ovine: SNAP29; lupine; RCAP 18; cathelicidin; antimicrobial;
KM	bactericidal; antibiotic; antiviral; microbial growth inhibitor;
KM	proliferation inhibitor; gene therapy; Pseudomonas aeruginosa;
KM	Burkholderia cepacia; Alcaligenes; Xanthomonas.
XX	
OS	Ovis aries.
XX	
PN	MO200112668-A1.
XX	
PD	22-FEB-2001.
XX	
PF	18-AUG-2000; 2000MO-US022781.
XX	
PR	18-AUG-1999; 99US-0149886P.
XX	
PA	(IOWA) UNIV IOWA RES FOUND.
PA	(REGC) UNIV CALIFORNIA.
XX	
PI	Tack BE, Mccrery P, Welsh M, Travis SM, Lehrner R;
XX	
DR	WPI; 2001-234911/24.
XX	
PT	New antimicrobial peptides useful as antibiotics for inhibiting growth
PT	and proliferation of microbes, and for treating microbial infections.
XX	
PS	Claim 1; Page 103; 137pp; English.
XX	
CC	AAE20848 to AAB70675 represent antimicrobial peptides (1), of which
CC	AAE20848 to AAB70664, AAB70674 and AAB70675 are derived from the ovine
CC	SNAP 29 cathelicidin family peptide, and AAB70665 to AAB70673 are derived
CC	from the lupine RCAP 18 cathelicidin family peptide. (1) have antibiotic,
CC	antimicrobial and antiviral activities, and can be used as microbial
CC	growth and proliferation inhibitors and in gene therapy. (1) are useful
CC	for inhibiting microbial growth in an environment capable of sustaining
CC	such growth, for inhibiting microbial growth or strain in a host, and
CC	inhibiting the growth of drug-resistant microbial strains such as
CC	Pseudomonas aeruginosa, Burkholderia cepacia, Alcaligenes and Xanthomonas
XX	